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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:30:07 ; Search time 28.382 Seconds
(without alignments)
2457.601 Million cell updates/sec

Title: US-09-807-933b-1
Perfect score: 1836
Sequence: 1 MKFTTASSALDALALGTEM.....TYKEVTPKPEITPAKTCGRK 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL 21:*
2: sp archaea:*
3: sp bacteria:*
4: sp fungi:*
5: sp human:*
6: sp invertebrate:*
7: sp mammal:*
8: sp mhc:*
9: sp organelle:*
10: sp phage:*
11: sp plant:*
12: sp rodent:*
13: sp virus:*
14: sp vertebrate:*
15: sp unclassified:*
16: sp ivirus:*
17: sp bacteriophage:*
18: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	778.5	42.4	219	14	Q9JH92
2	772.5	42.1	219	14	Q9JH91
3	772.5	42.1	220	14	Q9JH84
4	769.5	41.9	219	14	Q9JH87
5	767.5	41.8	220	14	Q9JH83
6	766.5	41.7	219	14	Q9JH89
7	763.5	41.6	217	14	Q9JH95
8	762.5	41.5	219	14	Q9JH90
9	761.5	41.4	219	14	Q9JH93
10	760.5	41.4	219	14	Q9JH88
11	755.5	41.1	219	14	Q9JH86
12	753.5	41.0	218	14	Q9JH94
13	743.5	40.5	220	14	Q9JH96
14	727.5	39.6	410	3	Q9P868
16	687	37.4	305	3	Q9J782

17	631	34.4	227	3	Q9J783	Q9J783 humicola gr
18	580.5	31.6	271	3	Q9UVP3	Q9UVP3 alternaria
19	568	30.9	242	5	Q97401	Q97401 phaedin coc
20	359.5	19.6	112	14	Q9JH90	Q9JH90 unclassified
21	358.5	19.5	112	14	Q9JH99	Q9JH99 unclassified
22	355.5	19.4	112	14	Q9JH98	Q9JH98 unclassified
23	346.5	18.9	112	14	Q9JH91	Q9JH91 unclassified
24	345.5	18.8	112	14	Q9JH92	Q9JH92 unclassified
25	340	18.5	111	14	Q9JH97	Q9JH97 unclassified
26	241	13.1	471	3	Q9HEV8	Q9HEV8 trichoderma
27	222	12.1	493	3	Q9P8D0	Q9P8D0 trichoderma
28	217	11.8	197	3	Q9P7F1	Q9P7F1 schizosacch
29	214.5	11.7	476	3	Q9C1S9	Q9C1S9 humicola in
30	204.5	11.1	439	3	Q92401	Q92401 agaricus bi
31	203.5	11.1	439	3	Q9P893	Q9P893 agaricus bi
32	200	10.9	345	3	Q9W217	Q9W217 penicillium
33	191.5	10.4	444	3	Q96VU2	Q96VU2 lentinula e
34	188.5	10.3	410	3	Q12665	Q12665 penicillium
35	188	10.2	418	3	Q93833	Q93833 trichoderma
36	186.5	10.2	457	3	Q93837	Q93837 acremonium
37	186.5	10.2	823	3	Q74203	Q74203 phanerocha
38	185.5	10.1	443	3	Q9C1R4	Q9C1R4 lentinula e
39	185.5	10.1	823	3	Q9URP5	Q9URP5 phanerocha
40	184	10.0	408	3	Q9HEZ1	Q9HEZ1 phanerocha
41	181	9.9	408	3	Q9HEZ2	Q9HEZ2 phanerocha
42	175	9.5	802	3	Q8TGC6	Q8TGC6 phanerocha
43	170.5	9.3	436	3	Q9P8N1	Q9P8N1 cortolus ve
44	170.5	9.3	460	3	Q02321	Q02321 phanerocha
45	164.5	9.0	290	3	Q9HEZ0	Q9HEZ0 phanerocha

ALIGNMENTS

RESULT 1

Q9JH92 PRELIMINARY; PRT; 219 AA.
AC Q9JH92;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
NCBI_Taxid=42452;
RX [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus."
DR Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB045171; BAA98041.1; --
DR HSSP; P43316; ZENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SO SEQUENCE 219 AA; 23001 MW; 5FZEB81A6DBE926CE CRC64;

QY	Query Match	42.4%	Score 778.5;	DB 14;	Length 219;
QY	Best Local Similarity	67.1%;	Pred. No. 1.6e-45;		
QY	Matches 139;	Conservative 25;	Mismatches 38;	Indels 5;	Gaps 3;
QY	132	NCVTTRYMDCKKASGSPKAVSSPKNDGVYAL-SDSNAOSGNGSGSYMNCNDQ	190		
QY	16	SRRTTRYMDCKKASGSPKAVSSPKNDGVYAL-SDSNAOSGNGSGSYMNCNDQ	75		
QY	191	PAVVDNLAVGPAALAAISGSGSRWCCSCEFLTFTSTVAGKKNVQVNTGDLGSSYTG	250		
QY	76	PAVVDNLAVGPAALAAISGSGSRWCCSCEFLTFTSTVAGKKNVQVNTGDLGSSYTG	132		
QY	251	AHPDLQMPGGGIVGIFNGSSQWGAIPNDGSGRYGIGSASDCLSPALQACCKRPNWF	310		
QY	133	-QFDLAPGGGIVGIVGCTGQSGAPADGWSRGGVSSRSCSOLPSGLQACCKRPNWF	191		

OY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 337
 Db 192 QNADNPSINPQVTCPEKITAKTNCGR 218

RESULT 2

O9JH91 PRELIMINARY; PRT; 219 AA.

AC O9JH91; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohnoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045172; BAA98042.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23126 MW; A112EF3FCAB041C CRC64;

Query Match 42.1%; Score 772.5; DB 14; Length 219;
 Best Local Similarity 66.7%; Pred. No. 4e-45;
 Matches 138; Conservative 26; Mismatches 38; Indels 5; Gaps 3;

OY 132 NGVTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNSYMCNDNQ 190
 Db 16 SGRTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNSYMCNDNQ 75
 OY 191 PMAVNDNLAYGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGDLSSTG 250
 Db 76 PMAVNDNLAYGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGDLSSTG 132
 OY 251 AHFDLQMPGGVGIIFNGCSSQWGPNDGMSRRYGGISASDCSSLPALQACKRRFMWF 310
 Db 133 -QFDLAIPEGGVGIYNGCTQOSGAPSDGMSRRYGGISASDCSSLPALQACKRRFMWF 191
 OY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 337
 Db 192 QNADNPSINPQVTCPEKITAKTNCGR 218

RESULT 3

O9JH84 PRELIMINARY; PRT; 220 AA.

AC O9JH84; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohnoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045179; BAA98049.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.

SQ SEQUENCE 220 AA; 23274 MW; 26AF5357512EA061 CRC64;

Query Match 42.1%; Score 772.5; DB 14; Length 220;
 Best Local Similarity 66.2%; Pred. No. 4e-45;
 Matches 137; Conservative 27; Mismatches 38; Indels 5; Gaps 3;

OY 132 NGVTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNSYMCNDNQ 190
 Db 17 SGRTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNSYMCNDNQ 76
 OY 191 PMAVNDNLAYGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGDLSSTG 250
 Db 77 PMAVNDNLAYGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGDLSSTG 133
 OY 251 AHFDLQMPGGVGIIFNGCSSQWGPNDGMSRRYGGISASDCSSLPALQACKRRFMWF 310
 Db 134 -QFDLAIPEGGVGIYNGCTQOSGAPSDGMSRRYGGISASDCSSLPALQACKRRFMWF 192
 OY 311 KNADNPSMTYKEVTCPEKITAKTGCGR 337
 Db 193 QNADNPSINPQVTCPEKITAKTNCGR 219

RESULT 4

O9JH87 PRELIMINARY; PRT; 219 AA.

AC O9JH87; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Family 45 cellulase homologue.
 OS unclassified eukaryotes.
 OC Eukaryota.
 OX NCBI_TaxID=42452;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ohnoko K., Ohkuma M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of termite Reticulitermes speratus.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045176; BAA98046.1; -
 DR HSSP; P43316; 2ENG.
 DR InterPro; IPR000334; GH 45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
 SQ SEQUENCE 219 AA; 23134 MW; 4BDEF4BC9ACC72D CRC64;

Query Match 41.9%; Score 769.5; DB 14; Length 219;
 Best Local Similarity 63.1%; Pred. No. 6.4e-45;
 Matches 135; Conservative 32; Mismatches 42; Indels 5; Gaps 3;

OY 125 VSGGASGVVTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNS 183
 Db 9 ISNGLADSGRTRYWDCCCKASGMPGKANVSPVSKCNKDGVTAL-SDSNAGSGCNGNS 68
 OY 184 YMCNDNPMANVNDNLAYGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGD 243
 Db 69 FMCDQTPVQVSSLSLGFAPAAALISGGSERWCCSCFELTFTSTVAGKMMVQVNTNGD 127
 OY 244 DLGSGTAHFDLQMPGGVGIIFNGCSSQWGPNDGMSRRYGGISASDCSSLPALQACG 303
 Db 128 DLGSGTAHFDLQMPGGVGIIFNGCSSQWGPNDGMSRRYGGISASDCSSLPALQACG 184
 OY 304 KRRFNFKNADNPSMTYKEVTCPEKITAKTGCGR 337
 Db 185 QMRFDMFQNADNPSINPQVTCPEKITAKTNCGR 218

RESULT 5

O9JH83 PRELIMINARY; PRT; 220 AA.

ID O9JH83; 01-OCT-2000 (Tremblrel. 15, Created)

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Query Match Similarity 41.7%; Score 766.5; DB 14; Length 219;
Best Local Similarity 64.7%; Pred. No. 16-44;
Matches 134; Conservative 29; Mismatches 39; Indels 5; Gaps 3

QY 132 NGVTRRYDDCCASGSPGKANVSSFPVKSCKNDGVTAL--SDSNAGSGCNGGNSYMCNDNQ 190
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 16 SKRTTRYYDCCGSGSGEMERKANVDRKIDTCADGQGVTRVSNPTVSGSCGGGCGFMYCDOT 75

```

RESULT 8		
Q9JH90		
ID	Q9JH90	PRELIMINARY; PRT; 219 AA.
AC	Q9JH90;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)	
DE	Family 45 cellulase homologue.	
OS	Unclassified eukaryotes.	
OC	Eukaryota.	
OX	NCBI_TaxID=42452;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Onocho K., Ohkuma M., Moriya S., Kudo T.:	
RT	"Diverse genes of family 45 cellulase homologues of the symbiotic	

Query Match	41.5%	Score 761.5;	DB 14;	Length 220;
Best Local Similarity	65.0%;	Pred. No. 2.2e-44;		
Matches 134;	Conservative 26;	Mismatches 41;	Indels 5;	Gaps 3
Qy	133	GVTTRYYDCCASGASGWPBGKANVSSPVKSCNMDGVTAI--SDSNAGSCNGGANSYWCNDNOP	191	
Db	18	GRTTRYYDCCGSGCMGKKANVDKPIDTCANDGTTTAVASNDYVAKSGCDGGDGMYWCYDQSP	77	
Qy	192	WAVNDNTLAYGFPAALAAISGGGSRMCCSCFELTFTSTVAGKKMYQVYNTNGDLDGSGTGA	251	
Db	78	WGVNDSEFLGFPAALAAVS--GGSEAACCMCYELTFTFSGPVGKKMYQVYNTNGDLSGN---	133	
Qy	252	HFDIQMPGGGAGVIFNGGSSQWGAPENDGWSRYGGIISASDSSLLPSALQACKKRREWFK	311	
Db	134	QFDLAIPEGGAGVIGYNGCTTAQSGAPADPDGWSRGVSSRSCECOLPSLGLOACQWRPFMFQ	193	
Qy	312	NADNPSSMYKEYETCPKELTAKTGCSR	337	
Db	194	NADNPISIFNNVSCPSSELIATKTNCR	219	

RN
 RP SEQUENCE FROM N.A.
 RA 11
 RA Ohtsuka K., Ohtsuka M., Moriya S., Kudo T.;
 RT "Diverse genes of family 45 cellulase homologues of the symbiotic
 RT protists in the hindgut of the termite *Reticulitermes speratus*.";
 RL Submitted (JUN-2000) to the EMBL/Genbank/DDBJ databases.
 DR EMBL; AB045177; BAA98047.1; -.
 DR HSSP; P43316; 2ENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS0140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
 SQ SEQUENCE 219 AA; 32158 MW; ECD868EABEDDD1 CRC64;

Query Match	Score	DB	Length
Best Local Similarity	Pred. No.		
41.1%;	755.5;	14;	219;
63.3%;	5.7e-4;		

